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RAW SEQUENCE LISTING

DATE: 10/02/2002

PATENT APPLICATION: US/09/868,131A

TIME: 09:42:05

Input Set : N:\Crf4\09232002\I868131.raw

Output Set: N:\CRF4\10022002\I868131A.raw

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1 <110> APPLICANT: Cohen, Philip
2     Kobayashi, Takayasu
3     Deak, Maria
4 <120> TITLE OF INVENTION: Methods
5 <130> FILE REFERENCE: 002.00160
6 <140> CURRENT APPLICATION NUMBER: US/09/868,131A
7 <141> CURRENT FILING DATE: 2002-07-31
8 <150> PRIOR APPLICATION NUMBER: PCT/GB99/04232
9 <151> PRIOR FILING DATE: 1999-12-14
10 <150> PRIOR APPLICATION NUMBER: GB 9919676.8
11 <151> PRIOR FILING DATE: 1999-08-19
12 <150> PRIOR APPLICATION NUMBER: US 60/112,217
13 <151> PRIOR FILING DATE: 1998-12-14
14 <160> NUMBER OF SEQ ID NOS: 44
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 367
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
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25         20             25             30
26     Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys
27         35             40             45
28     Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys
29         50             55             60
30     Val Leu Gln Lys Lys Ser Ile Leu Lys Lys Lys Glu Gln Ser His Ile
31         65             70             75             80
32     Met Ala Glu Arg Ser Val Leu Leu Lys Asn Val Arg His Pro Phe Leu
33         85             90             95
34     Val Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val
35         100            105            110
36     Leu Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu
37         115            120            125
38     Arg Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Val Ala
39         130            135            140
40     Ser Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu
41         145            150            155            160
42     Lys Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr
43         165            170            175
44     Asp Phe Gly Leu Cys Lys Glu Gly Val Glu Pro Glu Asp Thr Thr Ser

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45          180          185          190
46 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys
47          195          200          205
48 Glu Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu
49          210          215          220
50 Tyr Glu Met Leu His Gly Leu Pro Pro Phe Tyr Ser Gln Asp Val Ser
51          225          230          235          240
52 Gln Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly
53          245          250          255
54 Arg Thr Val Ala Ala Cys Asp Leu Leu Gln Ser Leu Leu His Lys Asp
55          260          265          270
56 Gln Arg Gln Arg Leu Gly Ser Lys Ala Asp Phe Leu Glu Ile Lys Asn
57          275          280          285
58 His Val Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg
59          290          295          300
60 Leu Thr Pro Pro Phe Asn Pro Asn Val Thr Gly Pro Ala Asp Leu Lys
61          305          310          315          320
62 His Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly
63          325          330          335
64 Cys Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe
65          340          345          350
66 Leu Gly Phe Ser Tyr Ala Pro Glu Asp Asp Asp Ile Leu Asp Cys
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74 <223> OTHER INFORMATION: Description of Artificial Sequence:synthetic
75 peptide
76 <400> SEQUENCE: 2
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78 1 5 10 15
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82 <212> TYPE: PRT
83 <213> ORGANISM: Mus musculus
84 <400> SEQUENCE: 3
85 Met Ala Ser Ser Pro Val Gly Val Pro Ser Pro Gln Pro Ser Arg Ala
86 1 5 10 15
87 Asn Gly Asn Ile Asn Leu Gly Pro Ser Ala Asn Pro Asn Ala Arg Pro
88 20 25 30
89 Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys
90 35 40 45
91 Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys
92 50 55 60
93 Val Leu Gln Lys Lys Ser Ile Leu Lys Asn Lys Glu Gln Asn His Ile
94 65 70 75 80
95 Met Ala Glu Arg Asn Val Leu Leu Lys Asn Val Arg His Pro Phe Leu

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96          85          90          95 •
97 Val Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val:
98          100          105          110
99 Leu Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu
100          115          120          125
101 Arg Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Thr Ala Glu Val Ala
102          130          135          140
103 Ser Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu
104          145          150          155          160
105 Lys Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr
106          165          170          175
107 Asp Phe Gly Leu Cys Lys Glu Cys Val Glu Pro Glu Glu Thr Thr Ser
108          180          185          190
109 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys
110          195          200          205
111 Glu Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu
112          210          215          220
113 Tyr Glu Met Leu His Gly Leu Pro Pro Phe Phe Asn Thr Asp Val Ala
114          225          230          235          240
115 Gln Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly
116          245          250          255
117 Arg Thr Val Ala Ala Cys Asp Leu Leu Gln Gly Leu Leu His Lys Asp
118          260          265          270
119 Gln Arg Gln Arg Leu Gly Ser Lys Glu Asp Phe Leu Asp Ile Lys Asn
120          275          280          285
121 His Met Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg
122          290          295          300
123 Leu Thr Pro Pro Phe Asn Pro Asn Val Glu Gly Pro Ala Asp Leu Lys
124          305          310          315          320
125 His Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly
126          325          330          335
127 Cys Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe
128          340          345          350
129 Leu Gly Phe Ser Tyr Ala Gln Asp Asp Asp Ile Leu Asp Ser
130          355          360          365
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133 <211> LENGTH: 429
134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 4
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139 Pro Asp Phe Ile Lys Gln Arg Arg Ala Gly Leu Asn Glu Phe Ile Gln
140          20          25          30
141 Asn Leu Val Arg Tyr Pro Glu Leu Tyr Asn His Pro Asp Val Arg Ala
142          35          40          45
143 Phe Leu Gln Met Asp Ser Pro Lys His Gln Ser Asp Pro Ser Glu Asp
144          50          55          60
145 Glu Asp Glu Arg Ser Ser Gln Lys Leu His Ser Thr Ser Gln Asn Ile

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146      65      70      75      80
147  Asn Leu Gly Pro Ser Gly Asn Pro His Ala Lys Pro Thr Asp Phe Asp
148      85      90      95
149  Phe Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val Leu Ala
150      100      105      110
151  Lys Arg Lys Leu Asp Gly Lys Phe Tyr Ala Val Lys Val Leu Gln Lys
152      115      120      125
153  Lys Ile Val Leu Asn Arg Lys Glu Gln Lys His Ile Met Ala Glu Arg
154      130      135      140
155  Asn Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His
156      145      150      155      160
157  Tyr Ser Phe Gln Thr Thr Glu Lys Leu Tyr Phe Val Leu Asp Phe Val
158      165      170      175
159  Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu Arg Ser Phe Pro
160      180      185      190
161  Glu His Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser Ala Leu Gly
162      195      200      205
163  Tyr Leu His Ser Ile Lys Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn
164      210      215      220
165  Ile Leu Leu Asp Ser Val Gly His Val Val Leu Thr Asp Phe Gly Leu
166      225      230      235      240
167  Cys Lys Glu Gly Ile Ala Ile Ser Asp Thr Thr Thr Phe Cys Gly
168      245      250      255
169  Thr Pro Glu Tyr Leu Ala Pro Glu Val Ile Arg Lys Gln Pro Tyr Asp
170      260      265      270
171  Asn Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr Glu Met Leu
172      275      280      285
173  Tyr Gly Leu Pro Pro Phe Tyr Cys Arg Asp Val Ala Glu Met Tyr Asp
174      290      295      300
175  Asn Ile Leu His Lys Pro Leu Ser Leu Arg Pro Gly Val Ser Leu Thr
176      305      310      315      320
177  Ala Trp Ser Ile Leu Glu Glu Leu Leu Glu Lys Asp Arg Gln Asn Arg
178      325      330      335
179  Leu Gly Ala Lys Glu Asp Phe Leu Glu Ile Gln Asn His Pro Phe Phe
180      340      345      350
181  Glu Ser Leu Ser Trp Ala Asp Leu Val Gln Lys Lys Ile Pro Pro Pro
182      355      360      365
183  Phe Asn Pro Asn Val Ala Gly Pro Asp Asp Ile Arg Asn Phe Asp Thr
184      370      375      380
185  Ala Phe Thr Glu Glu Thr Val Pro Tyr Ser Val Cys Val Ser Ser Asp
186      385      390      395      400
187  Tyr Ser Ile Val Asn Ala Ser Val Leu Glu Ala Asp Asp Ala Phe Val
188      405      410      415
189  Gly Phe Ser Tyr Ala Pro Pro Ser Glu Asp Leu Phe Leu
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192 <210> SEQ ID NO: 5

193 <211> LENGTH: 2146

194 <212> TYPE: DNA

195 <213> ORGANISM: Homo sapiens

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199   cagcctggga ggggccacac cctgaccatc cccctttatc ccttctgaga tgtttgttag 180
200   gaagtctggg tccaggggat atcatttctt gttccatcca tgcaggggtt gcttacctcg 240
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202   tgcctgaagc cctggatggg cggagctgac ccccaaacac caactctatc atgcctgctc 360
203   ctccctgtcc cccagagct gcctgatcat tgctacagaa tgaactctag cccagctggg 420
204   accccaagtc cacagccctc cagggccaat gggaacatca acctggggcc ttcagccaac 480
205   ccaaatgccc agcccacgga cttcgacttc ctcaaagtca tcggcaaagg gaactacggg 540
206   aaggtcctac tggccaagcg caagtctgat ggggcgttct atgcagtga ggtactacag 600
207   aaaaagtcca tcttaaagaa gaaagagcag agccacatca tggcagagcg cagtgtgctt 660
208   ctgaagaacg tgcggcacc cttcctcgtg ggctgcgct actccttcca gacacctgag 720
209   aagctctact tcgtgctcga ctatgtcaac gggggagagc tcttcttcca cctgcagcgg 780
210   gagcgccggt tcctggagcc cggggccagg ttctacgctg ctgaggtggc cagcgccatt 840
211   ggctacctgc actccctcaa catcatttac agggatctga aaccagagaa cattctcttg 900
212   gactgccagg gacacgtggt gctgacggat tttggcctct gcaaggaaagg ttagagacct 960
213   gaagacacca catccacatt ctgtggtacc cctgagtact tggcacctga agtgcttcgg 1020
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215   ctccatggcc tgcgcctct ctacagccaa gatgtatccc agatgtatga gaacattctg 1140
216   caccagccgc tacagatccc cggaggccgg acagtggccg cctgtgacct cctgcaaagc 1200
217   cttctccaca aggaccagag gcagcggctg ggctccaaag cagactttct tgagattaag 1260
218   aaccatgtat tcttcagccc cataaactg gatgacctgt accacaagag gctaactcca 1320
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220   caggaagctg tgtccaagtc cattggctgt acccctgaca ctgtggccag cagctctggy 1440
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222   tagaagagaa ggacctgtga aactactgag gccagctggt attagtaagg aattaccttc 1560
223   agctgctagg aagagcgact caaactaaca atggcttcaa cgagaagcag gtttattttt 1620
224   tccagcacat aaaagaaaaa taatgtttcg gaggccagga ctggcaggac aggtcatcag 1680
225   atactcagag gctgtatctc tgccctgcca accttgacaa atggcttcca atgttaggtt 1740
226   tgctacaaga tggttactgg agctctagct gcctattttg tgtttaggga agggaaaatg 1800
227   gaggaaaagg gagaagagca aagggcgctt ttaaagagct ttcccaaaag ctccccccaa 1860
228   tgacttttgc ttccatctca ctaaccaccc acccctacct ggaatggagg ctgggaaaatg 1920
229   tggcttattt gctgggtacg tgactatccc taataacaaa ggggttttga ccctaagaca 1980
230   ttaggggaga atgttgggtg ggcagccagc cctcttttac catagggcct cctggtgttt 2040
231   ggattttgat ctcaatgtgt aaaatgacag agatgtaaca agctcatagg gtatcaaat 2100
232   ctcttattgt tctatgttga aaaaaaaaaa aaaaaaaaaa aaaaaa 2146
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235 <211> LENGTH: 2404
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 6
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241   tataaagttc tggtttcagt gggaagaagt gaatggttt tcttcaggag atatgcagag 180
242   tttgataaac ttataacac tttaaaaaaa cagtttcctg ctatggccct gaagattcct 240
243   gccagagaaa tatttgggtg taattttgat ccagatttta ttaaacaag acgagcagga 300
244   ctaaacgaat tcattcagaa ctagttagg tatccagaac ttataacca tccagatgtc 360
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VERIFICATION SUMMARY

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